RAW SEQUENCE LISTING
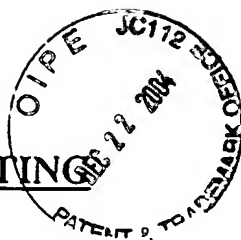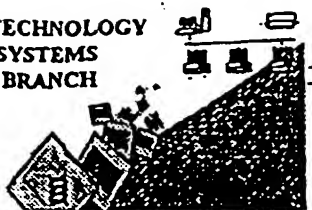## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/696,488
Source: TWO
Date Processed by STIC: 10-13-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *10/696,488*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1._____ Wrapped Nucleics Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .): this will prevent "wrapping."

2._____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3._____ Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4._____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5._____ Variable Length
Sequence(s)_____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing

6._____ PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)_____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7._____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences

8._____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9._____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10._____ Invalid <213> Response
Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11._____ Use of <220>
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)

12._____ PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13._____ Misuse of n/Xaa
"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING　　　　　　　　　DATE: 10/13/2004
PATENT APPLICATION:　　US/10/696,488　　TIME: 10:12:28

Input Set : A:\sequence listing-1-02.txt
Output Set: N:\CRF4\10132004\J696488.raw

```
  4 <110> APPLICANT: Cuenoud, Bernard
  5         Altmann, Karl-Heinz
  6         Martin, Pierre
  7         Moser, Heinz Ernst
  9 <120> TITLE OF INVENTION: 2'-Substituted Nucleosides and Oligonucleotide Derivatives
 11 <130> FILE REFERENCE: 4-20890B/C1
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/696,488
C--> 14 <141> CURRENT FILING DATE: 2003-10-29
 16 <150> PRIOR APPLICATION NUMBER: 09/194,844
 17 <151> PRIOR FILING DATE: 1999-05-14
 19 <150> PRIOR APPLICATION NUMBER: PCT/EP97/02738
 20 <151> PRIOR FILING DATE: 1998-05-27
 22 <150> PRIOR APPLICATION NUMBER: Switzerland 1432/96
 23 <151> PRIOR FILING DATE: 1996-06-06
```

<160> - please insert mandatory *(pg.1-4)*

numeric identifier <160> with response.

ERRORED SEQUENCES

```
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 20
 27 <212> TYPE: RNA
 28 <213> ORGANISM: Homo sapiens
E--> 0 <160> NUMBER OF SEQ ID NOS:
W--> 29 <400> SEQUENCE: 1
 30 aaugcauguc acaggcggga    20
 173 <210> SEQ ID NO: 14
 174 <211> LENGTH: 13
 175 <212> TYPE: DNA
 176 <213> ORGANISM: Artificial Sequence
W--> 177 <220> FEATURE:
W--> 178 <221> NAME/KEY: 2'-substituted sugar
 179 <222> LOCATION: 4, 6, 12
 180 <223> OTHER INFORMATION: Locations 4, 6, 12 = 2'-substituted sugar
W--> 181 <400> SEQUENCE: 14
E--> 182 aggtgtccgc atc    13
```

Pls see item # 11 on error summary sheet.

- Please explain source of genetic material.

Invalid Response

Type of errors shown exist throughout Sequence Listing. Please check subsequent sequences for similar errors

BEST AVAILABLE COPY

```
<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<221> phosphorothioate backbone
<222> 1-20
<221> 2'-substituted sugar
<222> 1-5 and 15-19
<223> Locations 1-20 = phosphorothioate backbone
      Locations 1-5 and 15-19 = 2'-substituted sugar
<400> 22
tcccgcctgt gacatgcatt                  20
```

VERIFICATION SUMMARY   DATE: 10/13/2004
PATENT APPLICATION: US/10/696,488   TIME: 10:12:29

Input Set : A:\sequence listing-1-02.txt
Output Set: N:\CRF4\10132004\J696488.raw

```
L:13  M:270 C: Current Application Number differs, Replaced Current Application Number
L:14  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0   M:282 E: Numeric Field Identifier Missing, <160> is required.
L:29  M:283 W: Missing Blank Line separator, <400> field identifier
L:36  M:283 W: Missing Blank Line separator, <220> field identifier
L:37  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:40  M:283 W: Missing Blank Line separator, <400> field identifier
L:47  M:283 W: Missing Blank Line separator, <220> field identifier
L:48  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:51  M:283 W: Missing Blank Line separator, <400> field identifier
L:58  M:283 W: Missing Blank Line separator, <220> field identifier
L:59  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:62  M:283 W: Missing Blank Line separator, <400> field identifier
L:69  M:283 W: Missing Blank Line separator, <220> field identifier
L:70  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:73  M:283 W: Missing Blank Line separator, <400> field identifier
L:80  M:283 W: Missing Blank Line separator, <220> field identifier
L:81  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:84  M:283 W: Missing Blank Line separator, <400> field identifier
L:91  M:283 W: Missing Blank Line separator, <220> field identifier
L:92  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:94  M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:98  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:98  M:283 W: Missing Blank Line separator, <400> field identifier
L:105 M:283 W: Missing Blank Line separator, <220> field identifier
L:106 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:108 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:112 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:112 M:283 W: Missing Blank Line separator, <400> field identifier
L:119 M:283 W: Missing Blank Line separator, <220> field identifier
L:120 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:122 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:126 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:126 M:283 W: Missing Blank Line separator, <400> field identifier
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:134 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:137 M:283 W: Missing Blank Line separator, <400> field identifier
L:144 M:283 W: Missing Blank Line separator, <220> field identifier
L:145 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:148 M:283 W: Missing Blank Line separator, <400> field identifier
L:155 M:283 W: Missing Blank Line separator, <220> field identifier
L:156 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:159 M:283 W: Missing Blank Line separator, <400> field identifier
L:166 M:283 W: Missing Blank Line separator, <220> field identifier
L:167 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:170 M:283 W: Missing Blank Line separator, <400> field identifier
L:177 M:283 W: Missing Blank Line separator, <220> field identifier
L:178 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
```

BEST AVAILABLE COPY

VERIFICATION SUMMARY   DATE: 10/13/2004
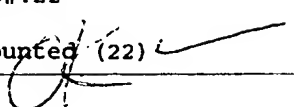PATENT APPLICATION: US/10/696,488   TIME: 10:12:29

Input Set : **A:\sequence listing-1-02.txt**
Output Set: **N:\CRF4\10132004\J696488.raw**

```
L:181 M:283 W: Missing Blank Line separator, <400> field identifier
L:182 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:188 M:283 W: Missing Blank Line separator, <220> field identifier
L:189 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:192 M:283 W: Missing Blank Line separator, <400> field identifier
L:199 M:283 W: Missing Blank Line separator, <220> field identifier
L:200 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:203 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:283 W: Missing Blank Line separator, <220> field identifier
L:211 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:214 M:283 W: Missing Blank Line separator, <400> field identifier
L:221 M:283 W: Missing Blank Line separator, <220> field identifier
L:222 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:224 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:228 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:228 M:283 W: Missing Blank Line separator, <400> field identifier
L:235 M:283 W: Missing Blank Line separator, <220> field identifier
L:236 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:238 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:242 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:242 M:283 W: Missing Blank Line separator, <400> field identifier
L:249 M:283 W: Missing Blank Line separator, <220> field identifier
L:250 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:252 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:256 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:256 M:283 W: Missing Blank Line separator, <400> field identifier
L:263 M:283 W: Missing Blank Line separator, <220> field identifier
L:264 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:266 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:270 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:270 M:283 W: Missing Blank Line separator, <400> field identifier
L:276 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:277 M:283 W: Missing Blank Line separator, <220> field identifier
L:278 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:280 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:284 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:284 M:283 W: Missing Blank Line separator, <400> field identifier
L:0 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (22)
```

BEST AVAILABLE COPY